



SEQUENCE LISTING

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Roberts, Nicholas J.
The Regents of the University of California

<120> LNP, a Protein Involved in the Initiation of
Mycorrhizal Infection in Plants

<130> 023070-079820US

<140> US 09/657,631

<141> 2000-09-06

<160> 14

<170> PatentIn Ver. 2.1

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<212> DNA

<213> Dolichos biflorus

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<221> CDS

<222> (51)..(1439)

<223> lectin nucleotide phosphohydrolase (LNP, NBP46 or
DB46) root lectin

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<222> (195)..(1436)

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Val His Val Phe Asn Phe Asp Gln Asn Leu Asp Leu Leu His Ile Gly
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aat gac ctc gag ttt aca aaa aag atc aaa ccc ggt ttg agc tca tac 344
Asn Asp Leu Glu Phe Thr Lys Lys Ile Lys Pro Gly Leu Ser Ser Tyr
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Ala Asp Lys Pro Glu Lys Ala Ala Glu Ser Leu Ile Pro Leu Leu Glu	
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Gly Lys Lys Tyr Asp Leu Tyr Val His Ser Tyr Leu Arg Tyr Gly Asn	
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cgt gac cta gct ctt cag att ctc aga ttg aat gag cca tgt tcc cat	1016
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 375 380 385
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 Ser Leu Pro Lys Phe Asn Arg Leu Met Tyr Phe Ile
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 <213> Dolichos biflorus

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 DB46) root lectin

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 Val Gly Asn Ser Ile Leu Leu Asn His Arg Lys Ile Leu Pro Asn Gln
 35 40 45
 Glu Leu Leu Thr Ser Tyr Ala Val Ile Phe Asp Ala Gly Ser Ser Gly
 50 55 60
 Ser Arg Val His Val Phe Asn Phe Asp Gln Asn Leu Asp Leu Leu His
 65 70 75 80

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Ser	Ser	Leu	Ser	Val	Gln	Pro	Asp	Ala	Val	Ser	Val	Ile	Asp	Gly	Thr		
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Gly	Glu	Ser	Tyr	Asn	Ile	Tyr	Gly	Pro	Thr	Ser	Gly	Ala	Asn	Phe	Asn		
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<220>

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<222> (1)..(1458)

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 root lectin

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      20               25               30

cta ctc act aat cga aag att ttc caa aaa caa gaa acc tta acc tct 144
Leu Leu Thr Asn Arg Lys Ile Phe Gln Lys Gln Glu Thr Leu Thr Ser
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tac gct gtc ata ttt gat gct ggt agc act ggt act cgt gtc cat gtt 192
Tyr Ala Val Ile Phe Asp Ala Gly Ser Thr Gly Thr Arg Val His Val
      50               55               60

tac cat ttt gat cag aac tta gat cta ctt cac att ggc aat gat att 240
Tyr His Phe Asp Gln Asn Leu Asp Leu Leu His Ile Gly Asn Asp Ile
      65               70               75               80

gag ttt gtt gac aag atc aaa cca ggt ttg agt gca tat ggg gat aat 288
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cct gaa caa gca gca aaa tct ctc att cca ctt ttg gag gaa gca gaa 336
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gat gtg gtt cct gag gat ctg cac ccc aaa aca ccc ctt agg ctt ggg 384
Asp Val Val Pro Glu Asp Leu His Pro Lys Thr Pro Leu Arg Leu Gly
      115              120              125

gca acc gca ggt ttg agg ctt ttg aat ggg gat gct gct gaa aag ata 432
Ala Thr Ala Gly Leu Arg Leu Leu Asn Gly Asp Ala Ala Glu Lys Ile
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caa cgt gat gca gtt tct att att gat gga acc caa gaa ggt tct tat 528
Gln Arg Asp Ala Val Ser Ile Ile Asp Gly Thr Gln Glu Gly Ser Tyr
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atg tgg gtg aca gtt aac tat gta ttg ggg aat ttg gga aaa agc ttc 576
Met Trp Val Thr Val Asn Tyr Val Leu Gly Asn Leu Gly Lys Ser Phe
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aca aaa tca gtg gga gta att gac ctt gga ggt ggt tca gtt caa atg 624
Thr Lys Ser Val Gly Val Ile Asp Leu Gly Gly Gly Ser Val Gln Met
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225 230 235 240	
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Tyr Asp Leu Tyr Val His Ser Tyr Leu Arg Phe Gly Lys Glu Ala Thr	
245 250 255	
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Arg Ala Gln Val Leu Asn Ala Thr Asn Gly Ser Ala Asn Pro Cys Ile	
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 root lectin

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Tyr His Phe Asp Gln Asn Leu Asp Leu Leu His Ile Gly Asn Asp Ile	
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Pro Glu Gln Ala Lys Ser Leu Ile Pro Leu Leu Glu Glu Ala Glu	
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Met Trp Val Thr Val Asn Tyr Val Leu Gly Asn Leu Gly Lys Ser Phe	
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Thr Lys Ser Val Gly Val Ile Asp Leu Gly Gly Gly Ser Val Gln Met	
195 200 205	
Thr Tyr Ala Val Ser Lys Lys Thr Ala Lys Asn Ala Pro Lys Val Ala	
210 215 220	
Asp Gly Glu Asp Pro Tyr Ile Lys Lys Leu Val Leu Lys Gly Lys Gln	
225 230 235 240	
Tyr Asp Leu Tyr Val His Ser Tyr Leu Arg Phe Gly Lys Glu Ala Thr	
245 250 255	
Arg Ala Gln Val Leu Asn Ala Thr Asn Gly Ser Ala Asn Pro Cys Ile	
260 265 270	
Leu Pro Gly Phe Asn Gly Thr Phe Thr Tyr Ser Gly Val Glu Tyr Lys	
275 280 285	
Ala Phe Ser Pro Ser Ser Gly Ser Asn Phe Asp Asp Cys Lys Glu Ile	
290 295 300	

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 305 310 315 320
 Thr Phe Gly Gly Ile Trp Asn Gly Gly Gly Ser Gly Gln Lys Lys
 325 330 335
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 370 375 380
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root lectin

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Phe Leu Ile Ser Leu Met Thr Phe Val Phe Met Leu Met Pro Ala Ile	
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35 40 45	
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Ser Gln Gln Pro Asn Thr Pro Val Lys Leu Gly Ala Thr Ala Gly Leu	
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Ser Ile Leu Asp Gly Thr Gln Glu Gly Ser Tyr Leu Trp Val Thr Ile	
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Asn Tyr Leu Leu Gly Lys Leu Gly Lys Arg Phe Thr Lys Thr Val Gly	
195 200 205	

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Val Val Asp Leu Gly Gly Gly Ser Val Gln Met Thr Tyr Ala Val Ser	
210 215 220	
agg aac aca gct aaa aat gct cca aaa gta cct gaa gga gag gat cca	720
Arg Asn Thr Ala Lys Asn Ala Pro Lys Val Pro Glu Gly Glu Asp Pro	
225 230 235 240	
tac ata aag aag ctt gta ctc cag gga aag aaa tat gac ctt tat gtt	768
Tyr Ile Lys Lys Leu Val Leu Gln Gly Lys Lys Tyr Asp Leu Tyr Val	
245 250 255	
cac agt tac ttg cgc tat gga aga gaa gca ttt cgt gca gag att ttc	816
His Ser Tyr Leu Arg Tyr Gly Arg Glu Ala Phe Arg Ala Glu Ile Phe	
260 265 270	
aag gtc gct ggt ggt tct gct aat cct tgc att tta gct ggc ttt gat	864
Lys Val Ala Gly Gly Ser Ala Asn Pro Cys Ile Leu Ala Gly Phe Asp	
275 280 285	
ggg gca tat aca tat tcc gga gca gag tat aag gtc tcg gcc cca gct	912
Gly Ala Tyr Thr Tyr Ser Gly Ala Glu Tyr Lys Val Ser Ala Pro Ala	
290 295 300	
tca gga tct aac ttg aat caa tgc aga aag ata gct ctt aag gct ctt	960
Ser Gly Ser Asn Leu Asn Gln Cys Arg Lys Ile Ala Leu Lys Ala Leu	
305 310 315 320	
aaa gtg aat gca cct tgt ccc tat cag aat tgc act ttt ggt ggg ata	1008
Lys Val Asn Ala Pro Cys Pro Tyr Gln Asn Cys Thr Phe Gly Gly Ile	
325 330 335	
tgg aat ggt gga ggt gga agt ggt caa aaa aat ctt ttc ctt act tca	1056
Trp Asn Gly Gly Gly Ser Gly Gln Lys Asn Leu Phe Leu Thr Ser	
340 345 350	
tct ttc tat tac ctc tct gaa gat gtt ggg atc ttt gtg aat aaa ccc	1104
Ser Phe Tyr Tyr Leu Ser Glu Asp Val Gly Ile Phe Val Asn Lys Pro	
355 360 365	
aat gcc aaa att cgt cca gtt gat ttg aag act gca gct aaa cta gct	1152
Asn Ala Lys Ile Arg Pro Val Asp Leu Lys Thr Ala Ala Lys Leu Ala	
370 375 380	
tgt aaa aca aat ctt gag gat gca aaa tcc aaa tac cca gat ctt tat	1200
Cys Lys Thr Asn Leu Glu Asp Ala Lys Ser Lys Tyr Pro Asp Leu Tyr	
385 390 395 400	
gag aaa gac agt gtt gaa tat gtg tgc ttg gat ctt gtc tac gtg tac	1248
Glu Lys Asp Ser Val Glu Tyr Val Cys Leu Asp Leu Val Tyr Val Tyr	
405 410 415	
aca ttg ctt gtt gat gga ttt ggt ctt gat cca ttt caa gag gtt aca	1296
Thr Leu Leu Val Asp Gly Phe Gly Leu Asp Pro Phe Gln Glu Val Thr	
420 425 430	
gtg gcg aat gaa att gaa tat cag gat gct ctt gtg gaa gcc gca tgg	1344
Val Ala Asn Glu Ile Glu Tyr Gln Asp Ala Leu Val Glu Ala Ala Trp	
435 440 445	

cct cta ggc act gcc ata gaa gca ata tca tca ttg cct aaa ttt gag 1392
 Pro Leu Gly Thr Ala Ile Glu Ala Ile Ser Ser Leu Pro Lys Phe Glu
 450 455 460

aga tta atg tat ttt att taa act act agt acc tgc tta agc ctg gat 1440
 Arg Leu Met Tyr Phe Ile Thr Thr Ser Thr Cys Leu Ser Leu Asp
 465 470 475 480

tac ctg aag aaa taa aat gaa ata aaa gcc gca tct ttc ttc ctt gct t 1489
 Tyr Leu Lys Lys Asn Glu Ile Lys Ala Ala Ser Phe Phe Leu Ala
 485 490 495

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<400> 9
 Lys Cys Ser Ser Leu Cys Ser
 1 5

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 root lectin

<400> 10
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 Val Phe Met Leu Met Pro Ala Ile Ser Ser Gln Tyr Leu Gly Asn
 20 25 30
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 35 40 45
 Val Thr Ser Tyr Ala Val Ile Phe Asp Ala Gly Ser Thr Gly Ser Arg
 50 55 60
 Val His Val Tyr Asn Phe Asp Gln Asn Leu Asp Leu Leu Pro Val Glu
 65 70 75 80
 Asn Glu Leu Glu Phe Tyr Asp Ser Val Lys Pro Gly Leu Ser Ser Tyr
 85 90 95
 Ala Ala Asn Pro Glu Glu Ala Ala Glu Ser Leu Ile Pro Leu Leu Lys
 100 105 110
 Glu Ala Glu Asn Val Val Pro Val Ser Gln Gln Pro Asn Thr Pro Val
 115 120 125
 Lys Leu Gly Ala Thr Ala Gly Leu Arg Leu Leu Glu Gly Asn Ala Ala
 130 135 140
 Glu Asn Ile Leu Gln Ala Val Arg Asp Met Leu Ser Asn Arg Ser Ala
 145 150 155 160
 Leu Asn Val Gln Ser Asp Ala Val Ser Ile Leu Asp Gly Thr Gln Glu
 165 170 175
 Gly Ser Tyr Leu Trp Val Thr Ile Asn Tyr Leu Leu Gly Lys Leu Gly
 180 185 190
 Lys Arg Phe Thr Lys Thr Val Gly Val Val Asp Leu Gly Gly Gly Ser
 195 200 205
 Val Gln Met Thr Tyr Ala Val Ser Arg Asn Thr Ala Lys Asn Ala Pro
 210 215 220

Lys Val Pro Glu Gly Glu Asp Pro Tyr Ile Lys Lys Leu Val Leu Gln
 225 230 235 240
 Gly Lys Lys Tyr Asp Leu Tyr Val His Ser Tyr Leu Arg Tyr Gly Arg
 245 250 255
 Glu Ala Phe Arg Ala Glu Ile Phe Lys Val Ala Gly Gly Ser Ala Asn
 260 265 270
 Pro Cys Ile Leu Ala Gly Phe Asp Gly Ala Tyr Thr Tyr Ser Gly Ala
 275 280 285
 Glu Tyr Lys Val Ser Ala Pro Ala Ser Gly Ser Asn Leu Asn Gln Cys
 290 295 300
 Arg Lys Ile Ala Leu Lys Ala Leu Lys Val Asn Ala Pro Cys Pro Tyr
 305 310 315 320
 Gln Asn Cys Thr Phe Gly Gly Ile Trp Asn Gly Gly Gly Gly Ser Gly
 325 330 335
 Gln Lys Asn Leu Phe Leu Thr Ser Ser Phe Tyr Tyr Leu Ser Glu Asp
 340 345 350
 Val Gly Ile Phe Val Asn Lys Pro Asn Ala Lys Ile Arg Pro Val Asp
 355 360 365
 Leu Lys Thr Ala Ala Lys Leu Ala Cys Lys Thr Asn Leu Glu Asp Ala
 370 375 380
 Lys Ser Lys Tyr Pro Asp Leu Tyr Glu Lys Asp Ser Val Glu Tyr Val
 385 390 395 400
 Cys Leu Asp Leu Val Tyr Val Tyr Thr Leu Leu Val Asp Gly Phe Gly
 405 410 415
 Leu Asp Pro Phe Gln Glu Val Thr Val Ala Asn Glu Ile Glu Tyr Gln
 420 425 430
 Asp Ala Leu Val Glu Ala Ala Trp Pro Leu Gly Thr Ala Ile Glu Ala
 435 440 445
 Ile Ser Ser Leu Pro Lys Phe Glu Arg Leu Met Tyr Phe Ile
 450 455 460

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 Thr Thr Ser Thr Cys Leu Ser Leu Asp Tyr Leu Lys Lys
 1 5 10

<210> 12
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 Asn Glu Ile Lys Ala Ala Ser Phe Phe Leu Ala
 1 5 10

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 PCR primer

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<223> n = g, a, c or t

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<222> (9)
<223> n = g, a, c or t

<400> 13
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20

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<220>
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PCR primer

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atrttrtada trccngg

17